

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2001, 13:56:10 : Search time 1546.09 seconds  
(without alignments)  
236.310 Million cell updates/sec

Title: US-09-869-185-1

Perfect score: 34  
Sequence: 1 gaagttctactcttctagagaataggacttc 34

Scoring table:

IDENTITY\_NUC  
Gapox 10.0, Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
22703874

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: em\_estfun:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estba:\*  
7: em\_estro:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: qd\_estcl:\*  
11: qd\_estl2:\*  
12: qd\_hic:\*  
13: qd\_gsa:\*  
14: em\_gsa\_fun:\*  
15: em\_gsa\_hum:\*  
16: em\_gsa\_inv:\*  
17: em\_gsa\_pin:\*  
18: em\_gsa\_pro:\*  
19: em\_gsa\_rtd:\*  
20: em\_gsa\_vrt:\*  
21: em\_gsa\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	34	100.0	81	10	A1265023 uk01f07.y
2	34	100.0	81	10	A1265111 uk03c08.y
3	34	100.0	81	10	A1272501 uk04g01.y
4	34	100.0	88	10	A1316311 u199a11.y
5	34	100.0	379	10	AV406802 AV406802
6	34	100.0	391	10	AV406859 AV406859
7	34	100.0	417	11	BF923935 OV4-NT025
8	34	100.0	446	13	AO502272 V6G7 mtm-
9	34	100.0	481	13	AO873999 V9F11 mtm
10	34	100.0	485	10	AU066556 AU066556
11	34	100.0	539	13	AQ378600 RPCI-11-1
12	33	97.1	458	10	AA305600 EST176597

C 13	32.4	95.3	725	13	AQ378598 RPCI-11-1
C 14	25	73.5	458	10	AA305600 EST176597
C 15	24.4	71.8	81	10	A1265023 uk01f07.y
C 16	24.4	71.8	81	10	A1265111 uk03c08.y
C 17	24.4	71.8	81	10	A1272501 uk04g01.y
C 18	24.4	71.8	88	10	A1316311 u199a11.y
C 19	24.4	71.8	379	10	AV406802 AV406802
C 20	24.4	71.8	391	10	AV406859 AV406859
C 21	24.4	71.8	417	11	BF923935 OV4-NT025
C 22	24.4	71.8	446	13	AO502272 V6G7 mtm-
C 23	24.4	71.8	481	13	AO873999 V9F11 mtm
C 24	24.4	71.8	485	10	AU066556 AU066556
C 25	24.4	71.8	539	13	AQ378600 RPCI-11-1
C 26	24.4	71.8	784	13	AQ491944
C 27	22.8	67.1	732	10	AA981255 V6G6e02.r
C 28	22.8	67.1	725	13	AQ378598 RPCI-11-1
C 29	22.4	65.9	231	10	BB234713 BB234713
C 30	21.8	64.1	949	13	CNS07AL7
C 31	21.6	63.5	188	10	AM231721
C 32	21.6	63.5	577	13	A2917497
C 33	21.4	62.9	414	11	BF548424
C 34	21.4	62.9	420	11	BF559634
C 35	21.4	62.9	446	11	BI395424
C 36	21.4	62.9	467	10	AM532666
C 37	21.4	62.9	481	10	BE103462
C 38	21.2	62.4	224	10	AV266987
C 39	21.2	62.4	314	10	BB548876
C 40	21.2	62.4	385	10	BE653729
C 41	21.2	62.4	389	10	AM321013
C 42	21.2	62.4	392	10	BE655029
C 43	21.2	62.4	493	10	BE289821
C 44	21.2	62.4	505	10	A1931732
C 45	21.2	62.4	527	10	A1891916

#### ALIGNMENTS

RESULT 1  
A1265023  
LOCUS  
DEFINITION  
uk01f07.y1 Schiller mouse MAC13 Mus musculus cDNA clone  
IMAGE:1958149 5', mRNA sequence.  
ACCESSION  
A1265023  
VERSION  
A1265023.1 GI:3883181  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheinberg, K., Stepien, M., Tan, F., Underwood, R., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.

TITLE  
JOURNAL  
COMMENT  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LBNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:984489  
Seq primer: -40RP from gibco.  
Location/Qualifiers  
1. 81  
/organism="Mus musculus"  
/db\_xref="taxon:10090"

FEATURES  
source

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/clone="IMAGE:1958149"
/clone_lib="Schiller mouse MAC13"
/tissue_type="colon cancer"
/cell_line="colon cancer cell line MAC13"
/lab_host="SOLR"
/note="Vector: plusscript SK- (Stratagene); Site_1: EcoRI
; Site_2: XhoI; Double-stranded cDNA was prepared from
cell line MAC13 using primer
5'-GAGAGAGAGAGAGAGAGAGAACTGCTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGACAGAG-3'. The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. This library
was constructed by Dr. Martin Schiller (Johns Hopkins
University)."
BASE COUNT      27 a      16 c      15 g      23 t
ORIGIN

Query Match      100.0%; Score 34; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 gaagttcctacattctcagagaatagaacttc 34
Db      17 GAAGTTCTCTACTTCTTAGAGAAATAGCACTTC 50

RESULT 2
LOCUS      A1265111      81 bp      mRNA      EST      18-NOV-1998
DEFINITION      UK03C08.Y1 Schiller mouse MAC13 Mus musculus cDNA clone
ACCESSION      IMAGE:1958318 5', mRNA sequence.
VERSION      A1265111
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 81)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HIMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HIMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:984658
Seq primer: -40RP from Gldco.

FEATURES
Source
1..81
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1958318"
/cell_line="Schiller mouse MAC13"
/tissue_type="colon cancer"
/cell_line="colon cancer cell line MAC13"
/lab_host="SOLR"
/note="Vector: plusscript SK- (Stratagene); Site_1: EcoRI
; Site_2: XhoI; Double-stranded cDNA was prepared from
cell line MAC13 using primer
5'-GAGAGAGAGAGAGAGAGAACTGCTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGACAGAG-3'. The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. This library
was constructed by Dr. Martin Schiller (Johns Hopkins
University)."
BASE COUNT      27 a      16 c      15 g      23 t
ORIGIN

Query Match      100.0%; Score 34; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 gaagttcctacattctcagagaatagaacttc 34
Db      17 GAAGTTCTCTACTTCTTAGAGAAATAGCACTTC 50

RESULT 3
LOCUS      A1272501      81 bp      mRNA      EST      18-NOV-1998
DEFINITION      UK04G01.Y1 Schiller mouse MAC13 Mus musculus cDNA clone
ACCESSION      IMAGE:1958448 5', mRNA sequence.
VERSION      A1272501
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 81)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HIMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HIMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:984768
Seq primer: Primer name ambiguous.

FEATURES
Source
1..81
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1958448"
/cell_line="Schiller mouse MAC13"
/tissue_type="colon cancer"
/cell_line="colon cancer cell line MAC13"
/lab_host="SOLR"
/note="Vector: plusscript SK- (Stratagene); Site_1: EcoRI
; Site_2: XhoI; Double-stranded cDNA was prepared from
cell line MAC13 using primer
5'-GAGAGAGAGAGAGAGAGAACTGCTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGACAGAG-3'. The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. This library
was constructed by Dr. Martin Schiller (Johns Hopkins
University)."
BASE COUNT      27 a      16 c      15 g      23 t
ORIGIN

Query Match      100.0%; Score 34; DB 10; Length 81;
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/db.xref="taxon:34305"  
/clone="MWL011d09\_r"  
/dev\_stage="young plants (two-week old)"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
XhoI; Isolate-MYakojima MC-20"

BASE COUNT 113 a 60 c 101 g 117 t  
ORIGIN

Query Match 100.0%; Score 34; DB 10; Length 391;  
Best Local Similarity 100.0%; Pred. NO. 0.0011;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaagtcctactctcagaagaataggaactc 34  
|||||  
Db 319 GAAGTTCCTATACCTTCTAGAGAAATAGCAACTTC 352

LOCUS 3935/c 417 bp mRNA EST 19-JAN-2001  
DEFINITION OVA-NT0251-251100-599-C04 NT0251 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF923935  
VERSION BF923935.1 GI:12319823  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 417)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL:  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1-QV4&l2-QV4-NT0251-  
251100-599-C04&l3-2000-11-25&l4-1)  
Seq primer: puc 18 forward  
High quality sequence stop: 417.

FEATURES  
source  
1. 417  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NT0251"  
/dev\_stage="Adult"  
/note="Organ: nervous\_tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent Application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT 121 a 106 c 70 g 120 t  
ORIGIN

Query Match 100.0%; Score 34; DB 11; Length 417;

Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaagtcctactctcagaagaataggaactc 34  
|||||  
Db 172 GAAGTTCCTATACCTTCTAGAGAAATAGCAACTTC 139

RESULT 8  
LOCUS AO502272 446 bp DNA GSS 29-APR-1999  
DEFINITION V667 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae  
genomic 5', DNA sequence.  
ACCESSION AO502272  
VERSION AO502272.1 GI:4707922  
KEYWORDS GSS.  
SOURCE baker's yeast.  
ORGANISM Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (bases 1 to 446)  
Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,  
desEtages, S.A., Cheung, K.-H., Sheehan, A., Symonakis, D., Jansen, R.,  
Umansky, L., Heidman, M., Nelson, K., Iwasa, H., Kanada, D., Lugo, R.,  
Hager, K., Miller, P., Roeder, G.S. and Snyder, M.  
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and  
Gene Disruption  
Unpublished (1999)  
CONTACT: Kumar A  
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology  
Yale University  
P.O. Box 208103, New Haven, CT 06520-8103, USA  
Tel: 203 432 9949  
Fax: 203 432 6161  
Email: anuj.kumar@yale.edu  
te of mTn-3xHA/lacZ insertion.  
Seq primer: GGCCCTCTCTTGGAGATAC  
Class: transposon-tagged.

TITLE  
JOURNAL -  
COMMENT Contact: Kumar A  
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology  
Yale University  
P.O. Box 208103, New Haven, CT 06520-8103, USA  
Tel: 203 432 9949  
Fax: 203 432 6161  
Email: anuj.kumar@yale.edu  
te of mTn-3xHA/lacZ insertion.  
Seq primer: GGCCCTCTCTTGGAGATAC  
Class: transposon-tagged.

FEATURES  
source  
1. 446  
Location/Qualifiers  
/organism="Saccharomyces cerevisiae"  
/db\_xref="taxon:4932"  
/clone\_lib="mTn-3xHA/lacZ Insertion Library"  
/lab\_host="E. coli"  
/note="Vector: pHS56-Sal; A yeast genomic DNA library  
(lacking mitochondrial DNA) was prepared in pHS56-Sal;  
genomic DNA was size-fractionated (DNA of roughly 2-3 kb  
in length) prior to cloning. This library was  
subsequently mutagenized with a mTn-3xHA/lacZ  
multitransposon containing lacZ, URA3, and tet resistance."

Query Match 100.0%; Score 34; DB 13; Length 446;  
Best Local Similarity 100.0%; Pred. NO. 0.0011;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaagtcctactctcagaagaataggaactc 34  
|||||  
Db 224 GAAGTTCCTATACCTTCTAGAGAAATAGCAACTTC 257

RESULT 9  
LOCUS AO873999/c 481 bp DNA GSS 08-NOV-1999  
DEFINITION V6F11 mTn-3xHA/lacZ Insertion Library, strain AB972 Saccharomyces  
cerevisiae genomic 5', DNA sequence.  
ACCESSION AO873999  
VERSION AO873999.1 GI:6286243  
KEYWORDS GSS.  
SOURCE baker's yeast.  
ORGANISM Saccharomyces cerevisiae

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
1 (bases 1 to 481)  
Ross-Macdonald, P., Roemer, T., Coelho, P. S. R., Agarwal, S., Kumar, A.,  
desBanges, S. A., Cheung, K. H., Sheehan, A., Symonakis, D., Jansen, R.,  
Umanskiy, L., Heidman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R.,  
Hager, K., Miller, P., Roeder, G. S. and Snyder, M.  
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and  
Gene Disruption  
Unpublished (1999)  
Contact: Kumar A  
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology  
Yale University  
P.O. Box 208103, New Haven, CT 06520-8103, USA  
Tel: 203 432 9949  
Fax: 203 432 6161  
Email: anuj.kumarey@yale.edu  
Le of mtb-3xHA/lacZ insertion.  
Seq primer: GGCCTCTCTTCTTGGAGATGAC  
Class: transposon-tagged.

TURES  
source  
Location/Qualifiers  
1. 481  
/organism="Saccharomyces cerevisiae"  
/strain="AB972 - trp1 r(0) (S288C background)"  
/db\_xref="taxon:4932"  
/clone\_id="mtb-3xHA/lacZ Insertion Library, strain AB972"  
/lab\_host="E. coli"  
/note="Vector: pHS56-Sal; A yeast genomic DNA library was  
prepared in pHS56-Sal; genomic DNA was size-fractionated  
(DNA of roughly 2-3 kb in length) prior to cloning. This  
library was subsequently mutagenized with a mtb-3xHA/lacZ  
multitransposon containing lacZ, URA3, and tet resistance."

BASE COUNT 135 a 126 c 85 g 132 t 3 others  
ORIGIN

Query Match 100.0%; Score 34; DB 13; Length 481;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaagtcctactctctagagaatagaacttc 34  
|||||  
Db 274 GAAGTCTCTATCTTCTCAGAGATAGCAACTTC 241

RESULT 10  
A0066556 485 bp mRNA EST 04-AUG-2000  
A0066556 Chlamydomonas sp. HS-5 lambda ZAP II Chlamydomonas sp.  
HS-5 cDNA clone PQ1, mRNA sequence.  
A0066556  
A0066556.1 GI:6448321  
EST.  
Chlamydomonas sp. HS-5.  
Chlamydomonas sp. HS-5.  
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadales; Chlamydomonas.  
1 (bases 1 to 485)  
Miyasaka, H., Kanaboshi, H. and Ikeda, K.  
Isolation of several anti-stress genes from halotolerant green alga  
Chlamydomonas by a simple functional expression screening in E. coli  
Unpublished (1999)  
Contact: Kazunori Ikeda  
Environmental Symbiosis section  
Kansai Environmental Engineering Center Co. Ltd  
3-5 Adzuchi-machi 1-Chome Chuo-ku, Osaka, Osaka 541-0052, Japan  
Email: daikemb@infoweb.ne.jp  
paragat inducible;  
Present address: The Kansai Electric Power Co., Technical Research  
Center, Bio-Laboratory, Nakoji 3-Chome 11-20, Amagasaki, Hyogo  
661-0974, Japan.  
Location/Qualifiers

FEATURES

source  
1. 485  
/organism="Chlamydomonas sp. HS-5"  
/strain="HS-5"  
/db\_xref="taxon:108458"  
/clone="PQ1"  
/clone\_id="Chlamydomonas sp. HS-5 lambda ZAP II"  
/note="Vector: lambda ZAP II; The cDNA clone was isolated  
from the halotolerant green alga Chlamydomonas HS-5 by a  
functional expression screening in E. coli cells. The  
principle of the screening method was based on the  
acquisition of stress tolerance of the bacterial cells  
carrying the cDNA."

BASE COUNT 139 a 88 c 118 g 140 t  
ORIGIN

Query Match 100.0%; Score 34; DB 10; Length 485;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaagtcctactctctagagaatagaacttc 34  
|||||  
Db 325 GAAGTCTCTATCTTCTCAGAGATAGCAACTTC 358

RESULT 11  
A0378600 539 bp DNA GSS 29-JUN-1999  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

A0378600  
RC11-11-161C8.TV RC11-11 Homo sapiens genomic clone RC11-11-161C8,  
DNA sequence.  
A0378600  
A0378600.1 GI:4349623  
GSS.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 539)  
Zhao, S., Adams, M. D., Nierman, W., Malek, J., de Jong, P. and Venter  
, J. C.  
Use of BAC End Sequences from Library RC11-11 for Sequence-Ready  
Map Building  
Unpublished (1997)  
Other-GSS: RC11-11-161C8.TJ  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeetlgr.org  
Clones are derived from the human BAC library RC11-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@jeong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page:  
[http://www.tlgr.org/tldb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html)  
Seq primer: T7  
Class: BAC ends.

FEATURES  
source  
1. 539  
/organism="Homo sapiens"  
/db\_xref="GDB:7561495"  
/db\_xref="taxon:9606"  
/clone="RC11-11-161C8"  
/clone\_id="RC11-11"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/note="Vector: pAC3.6, Site\_1: EcoRI; Site\_2: EcoRI;  
RC111 Human Male BAC Library"

BASE COUNT 160 a 91 c 133 g 155 t  
ORIGIN

Query Match 100.0%; Score 34; DB 13; Length 539;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gaagttctactactctctagagaatagaacttc 34  
 |||  
 Db 334 GAAGTTCTACTACTTTCTAGAGATAGCACTTC 367

## RESULT 12

AA305600

LOCUS 458 bp mRNA EST 18-APR-1997  
 DEFINITION EST176597 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA  
 5' end, mRNA sequence.

ACCESSION AA305600.1 GI:1957925

VERSION AA305600.1 GI:1957925

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 458)

AUTHORS Adams, M.D., Kervatage, A.R., Fleischmann, R.D., Fulmer, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, R.G., Gocayne, J.D., White, C., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Oline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geophagen, N.S., Glodde, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-T., Maratos-Flier, S.M., Merrick, J.N., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Benharik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferlie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Welsner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
 MEDLINE 96026280

COMMENT Contact: Kervatage, AR

Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423

Email: arkerlat@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source

1. 458  
 /organism="Homo sapiens"  
 /db\_xref="ATCC (inhost):129043"  
 /db\_xref="taxon:9606"  
 /clone\_11b="Colon carcinoma (Caco-2) cell line II"  
 /sex="male"  
 /tissue\_type="colon"  
 /cell\_type="Caco-2"  
 /note="Organ: colon; Vector: pluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"  
 EcoRI: 77 c 115 g 129 t 5 others

BASE COUNT 132 a 132 c 129 t 5 others  
 ORIGIN

Query Match 97.1%; Score 33; DB 10; Length 458;  
 Best Local Similarity 97.1%; Pred. No. 0.0027;

Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 gaagttctactactctctagagaatagaacttc 34  
 |||  
 Db 325 GAAGTTCTACTACTTTCTAGAGATAGCACTTC 358

## RESULT 13

AQ378598/C

LOCUS 725 bp DNA GSS 29-JUN-1999  
 DEFINITION RPCI-11-161C8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-161C8,  
 DNA sequence.

ACCESSION AQ378598

VERSION AQ378598.1 GI:4349621

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 725)

AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

JOURNAL Unpublished (1997)

COMMENT Other\_GSSs: RPCI-11-161C8.TV

Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: hbe@tigr.org  
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (<http://inforesgen.com>). BAC end search page: [http://www.tigr.org/tldb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html)  
 Seq primer: SP6  
 Class: BAC ends.

FEATURES Location/Qualifiers

source

1. 725  
 /organism="Homo sapiens"  
 /db\_xref="GDB:7561495"  
 /db\_xref="taxon:9606"  
 /clone="RPCI-11-161C8"  
 /clone\_11b="RPCI-11"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI; RPCI11 Human Male BAC Library"  
 BASE COUNT 237 a 144 c 152 g 192 t  
 ORIGIN

Query Match 95.3%; Score 32.4; DB 13; Length 725;  
 Best Local Similarity 97.1%; Pred. No. 0.005;  
 Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 gaagttctactactctctagagaatagaacttc 34  
 |||  
 Db 701 GAAGTTCTTAACCTTTCTAGAGATAGCACTTC 668

## RESULT 14

AA305600/C

LOCUS 458 bp mRNA EST 18-APR-1997  
 DEFINITION EST176597 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA  
 5' end, mRNA sequence.

ACCESSION AA305600.1 GI:1957925

KEYWORDS EST.

**SOURCE** human.  
**ORGANISM** Homo sapiens.  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**AUTHORS** 1 (bases 1 to 458)  
 Adams,M.D., Kerlavage,A.R., Fletschmann,R.D., Fuldner,R.A., Bult  
 C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White  
 O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Val,C., Clayton,R.A.,  
 Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald  
 L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A.,  
 Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,  
 Kelley,C.L., Liu,L.-I., Marrao,S.M., Merrick,J.M.,  
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dinke,D., Feng,D.-F., Fertle,A., Fischer,C., Hastings,G.A., He,M.W.,  
 Hu,Y.S., Hunge,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,  
 Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L.,  
 Wei,Y.F., Wang,Y., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon  
 M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and  
 Venter,J.C.  
**TITLE** Initial assessment of human gene diversity and expression patterns  
 based upon 832 million nucleotides of cDNA sequence  
**JOURNAL** Nature 377 (6547 Suppl.), 3-174 (1995)  
**MEDLINE** 96026280  
**COMMENT** Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse  
**FEATURES**  
**SOURCE** Location/Qualifiers  
 1..458  
 /organism="Homo sapiens"  
 /db\_xref="ATCC (Inhost):129043"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Colon carcinoma (Caco-2) cell line II"  
 /sex="male"  
 /tissue\_type="colon"  
 /cell\_type="Caco-2"  
 /cell\_line="Human colon adenocarcinoma;ATCC HTB 37"  
 /note="Organ: colon; Vector: plusscript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"  
**GC COUNT** 132 a 77 c 115 g 129 t 5 others  
**ORIGIN**  
 Query Match 73.5%; Score 25; DB 10; Length 458;  
 Best Local Similarity 82.4%; Pred. No. 4.7;  
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Oy 1 gaagttctatacttctagagaatagaacttc 34  
 ||||||||| | | | |||||||||  
 Db 358 GAAGTTCCTATCTCTANAAAGTATAGCAATTC 325  
**RESULT** 15  
**LOCUS** AI265023  
**DEFINITION** AI265023 81 bp mRNA EST 18-NOV-1998  
 uk010f.y1 Schiller mouse MAC13 Mus musculus cDNA clone  
**IMAGE**:1958149 5', mRNA sequence.  
**ACCESSION** AI265023  
**VERSION** AI265023.1 GI:3683181  
**KEYWORDS** EST.  
**SOURCE** house mouse.  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
1 (bases 1 to 81)
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE
The Mashu-HHMI Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
Mashu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:984469
Seq primer: -40RP from Glbco.
FEATURES
SOURCE
location/Qualifiers
1..81
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_image="1958149"
/clone_lib="Schiller mouse MAC13"
/tissue_type="colon cancer"
/cell_line="colon cancer cell line MAC13"
/lab_host="SOLR"
/note="Vector: pBluescript SK- (Stratagene); Site_1: EcoRI
; Site_2: XhoI; Double-stranded cDNA was prepared from
cell line MAC13 using primer
5'-GAGAGAGAGAGAGAGAGAGAGAGTGTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGACGACGAG-3'. The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. This library
was constructed by Dr. Martin Schiller (Johns Hopkins
University)."
BASE COUNT
27 a 16 c 15 g 23 t
ORIGIN
Query Match 71.8%; Score 24.4; DB 10; Length 81;
Best Local Similarity 82.4%; Pred. No. 7.2;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 gaagttcctatacttctagagaatagaacttc 34
|||||
Db 50 GAAGTTCCATATCTCTAGAAAGTATAGGAACATTC 17

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2001, 14:22:45 : Search time 164.07 Seconds  
(without alignments)  
177.662 Million cell updates/sec

Title: US-09-869-185-1

Perfect score: 34  
Sequence: 1 gaagtcctatcttcttagaagaagacttc 34

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

11 number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N.Geneseq\_1101:\*

- 1: /SIDSR/gcgdata/geneseq/geneseq/NA1980.DAT.\*
- 2: /SIDSR/gcgdata/geneseq/geneseq/NA1981.DAT.\*
- 3: /SIDSR/gcgdata/geneseq/geneseq/NA1982.DAT.\*
- 4: /SIDSR/gcgdata/geneseq/geneseq/NA1983.DAT.\*
- 5: /SIDSR/gcgdata/geneseq/geneseq/NA1984.DAT.\*
- 6: /SIDSR/gcgdata/geneseq/geneseq/NA1985.DAT.\*
- 7: /SIDSR/gcgdata/geneseq/geneseq/NA1986.DAT.\*
- 8: /SIDSR/gcgdata/geneseq/geneseq/NA1987.DAT.\*
- 9: /SIDSR/gcgdata/geneseq/geneseq/NA1988.DAT.\*
- 10: /SIDSR/gcgdata/geneseq/geneseq/NA1989.DAT.\*
- 11: /SIDSR/gcgdata/geneseq/geneseq/NA1990.DAT.\*
- 12: /SIDSR/gcgdata/geneseq/geneseq/NA1991.DAT.\*
- 13: /SIDSR/gcgdata/geneseq/geneseq/NA1992.DAT.\*
- 14: /SIDSR/gcgdata/geneseq/geneseq/NA1993.DAT.\*
- 15: /SIDSR/gcgdata/geneseq/geneseq/NA1994.DAT.\*
- 16: /SIDSR/gcgdata/geneseq/geneseq/NA1995.DAT.\*
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- 19: /SIDSR/gcgdata/geneseq/geneseq/NA1998.DAT.\*
- 20: /SIDSR/gcgdata/geneseq/geneseq/NA1999.DAT.\*
- 21: /SIDSR/gcgdata/geneseq/geneseq/NA2000.DAT.\*
- 22: /SIDSR/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	18- AAT92196	S. cerevisiae FRT
2	34	100.0	34	19- AAV43562	FLP recombinase ta
3	34	100.0	34	20- AAV72331	Wild type FRT site
4	34	100.0	34	20- AAV61227	Wild type FRT site
5	34	100.0	34	20- AAX01426	2mu FRT element, e
6	34	100.0	34	21- AAC61513	Nucleotide sequenc
7	34	100.0	34	21- AAC63090	Wild-type FRT site
8	34	100.0	34	21- AAA10237	FLP recombination
9	34	100.0	34	21- AA58072	FLP recombinase ta
10	34	100.0	34	22- AAD10220	Minimal wild-type
11	34	100.0	34	22- AAH21799	Saccharomyces FRT

C 12	34	100.0	34	22	AAF81218	FLP recombinase re
C 13	34	100.0	34	22	AAF24488	FLP recombination
C 14	34	100.0	34	22	AAF87355	Yeast FRT sequence
C 15	34	100.0	35	20	AAZ06422	FLP recombinase ta
C 16	34	100.0	36	22	AAH21812	Saccharomyces FRT
C 17	34	100.0	40	22	AAH21809	Saccharomyces FRT
C 18	34	100.0	40	22	AAH21810	Saccharomyces FRT
C 19	34	100.0	44	22	AAH21811	Saccharomyces FRT
C 20	34	100.0	48	20	AAZ06421	FLP recombinase ta
C 21	34	100.0	48	21	AAZ06429	Wild-type FRT site
C 22	34	100.0	48	21	AAZ06448	FLP site, Unident
C 23	34	100.0	48	21	AAZ06430	FRT site-specific
C 24	34	100.0	52	22	AAF87366	Oligonucleotide ba
C 25	34	100.0	52	22	AAF87367	Oligonucleotide ba
C 26	34	100.0	54	15	AAZ06429	Complete FRT site
C 27	34	100.0	54	20	AAZ06429	Oligonucleotide HR
C 28	34	100.0	54	20	AAZ06430	Oligonucleotide HR
C 29	34	100.0	54	20	AAZ06431	Oligonucleotide HR
C 30	34	100.0	54	20	AAZ06432	Oligonucleotide HR
C 31	34	100.0	54	20	AAZ06423	Oligonucleotide 47
C 32	34	100.0	54	20	AAZ06424	Oligonucleotide 47
C 33	34	100.0	54	20	AAZ27788	Full length FRT si
C 34	34	100.0	54	21	AAZ37987	FLP recognition se
C 35	34	100.0	54	22	AAF87387	Yeast FLP recognit
C 36	34	100.0	59	22	AAZ06431	DNA encoding seque
C 37	34	100.0	61	19	AAZ20355	FLP recombination
C 38	34	100.0	69	20	AAZ23332	FRT variant site
C 39	34	100.0	69	20	AAZ61228	Mutant FRT site, F
C 40	34	100.0	69	22	AAF24489	FLP recombinase
C 41	34	100.0	81	22	AAZ06425	DNA encoding seque
C 42	34	100.0	96	20	AAZ06425	Oligonucleotide 47
C 43	34	100.0	96	20	AAZ06426	Oligonucleotide 47
C 44	34	100.0	123	20	AAZ87476	Plasmid pAAK705 PC
C 45	34	100.0	130	20	AAZ87475	Plasmid pAAK705 PC

#### ALIGNMENTS

RESULT 1

AAZ92196 standard: DNA: 34 BP.

AC AAT92196:

XX 06-FEB-1998 (first entry)

XX S. cerevisiae FRT recombination site.

XX Replication-defective recombinant viral vector: helper virus: deletion;

KM encapsidation; propagation; recombination; bacteriophage P1; loxP; FRT;

KM Saccharomyces cerevisiae; Zygosaccharomyces rouxii; site R; recombinase;

KW complementation cell line; CRE; viral particle; gene therapy; human;

KW cellular therapy; ss.

XX Saccharomyces cerevisiae.

OS

XX

PN W09705255-A2.

XX

PD 13-FEB-1997.

XX

PF 30-JUL-1996; 96MO-FR01200.

XX

PR 31-JUL-1995; 95FR-0009289.

XX

PA (TRGE ) TRANSGENE SA.

XX

PI Lusk M, Mehtali M;

XX WPI; 1997-145692/13.

DR

XX

PT Helper virus contg. sequences recognised by recombinase, flanking

essential region - useful for producing viral particles enriched

PT for replication-deficient viral vectors, esp. for gene therapy  
XX Disclosure; Page 28; 44pp; French.  
XX  
CC The invention relates to the production of replication-defective  
CC recombinant viral vector (RVV) by producing a helper virus (HV) in  
CC which a region essential, especially the encapsidation region, for  
CC HV propagation is deleted, preferably by recombination between 2  
CC recombination sites flanking the essential region. Examples of  
CC recombination sequences useful for generating the HV include the  
CC bacteriophage P1 loxP sequence (AA92195), the Saccharomyces cerevisiae  
CC FRT sequence (presented here) or the Zygosaccharomyces rouxii site R  
CC (AA92197). The RVV and HV are preferably introduced into a  
CC complementation cell line comprising a DNA fragment coding for a  
CC recombinase, especially the FLP protein if the FRT site is used.  
CC The new helper virus is able to express the genes it carries, i.e. to  
CC complement a gene which is deficient in RVV, but HV cannot be propagated  
CC in the presence of recombinase. The viral particles are particularly  
CC useful for gene and cellular therapy in humans.  
Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;  
Query Match 100.0%; Score 34; DB 18; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gaagttcctatacttctagaagaataggaaacttc 34  
Db 1 gaagttcctatacttctagaagaataggaaacttc 34  
RESULT 2  
AAV43562/c  
ID AAV43562 standard; DNA: 34 BP.  
XX  
AC AAV43562;  
XX  
DT 16-SEP-1998 (first entry)  
XX  
DE FLP recombinase target FRT site.  
XX  
KW Tagged gene; tagged transcript; hybrid intron; protein tag;  
KW protein isolation; recombination; subcellular structure analysis;  
KW transcriptional regulation; viral infection; FLP recombinase; ss.  
XX  
OS Unidentified.  
XX  
MO9820031-A1.  
PD 14-MAY-1998.  
XX  
PF 07-NOV-1997; 97WO-US20150.  
XX  
PR 08-NOV-1996; 96US-0705404.  
XX  
PA (JARV/) JARVik J W.  
XX  
PI Jarvik JW;  
XX  
DR WPI: 1998-266861/25.  
XX  
PT Tagging genes, transcripts and proteins - using tag-creating DNA  
PT inserted into intron of gene to create 2 hybrid introns separated by  
PT new exon encoding protein tag  
XX  
PS Disclosure; Page 19; 66pp; English.  
XX  
CC This represents the target FRT site of FLP recombinase, a site-specific  
CC recombination system used for altering the expression and function of  
CC CD-tagged genes. The invention provides methods for tagging genes,  
CC transcripts and proteins in cells in a single recombination event. The  
CC method comprises producing a tagged gene by inserting a DNA sequence

CC into an intron of a gene by selecting a DNA sequence having a 5' portion  
CC free of any nucleotide sequence selected from AAV43548 to AAV43551, a  
CC nucleotide sequence selected from AAV43552 to AAV43560 and nucleotide  
CC sequences identical to a known splice branch site in a known gene,  
CC sequences identical in length to a known spacer region between splice  
CC branch and acceptor sites in a known gene, sequences identical to a known  
CC splice acceptor site in a known gene, sequence identical to a known  
CC splice donor site in a known gene, an open reading frame (ORF) 3N-1  
CC nucleotides in length, the ORF encoding a known peptide tag and sequences  
CC by a known reaction characteristic of the known peptide tag and sequences  
CC selected from CAGG and TAGG. The DNA sequence is inserted into the intron  
CC within the gene to create a tagged gene, and the tagged gene is incubated  
CC within a cell so as to maintain intact or to introduce the tagged gene  
CC within the genome of the cell. The method is used for isolating proteins,  
CC RNA and genes, for analysis of subcellular structures, cellular responses  
CC and transcriptional regulation, for the study of viral infection and for  
CC diagnosis of disease.  
XX  
SQ Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;  
Query Match 100.0%; Score 34; DB 19; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 gaagttcctatacttctagaagaataggaaacttc 34  
Db 34 GAAGTTCCTATCTTCTAGAGAAATAGCAACTTC 1  
RESULT 3  
AAV72331/c  
ID AAV72331 standard; DNA: 34 BP.  
XX  
AC AAV72331;  
XX  
DT 28-JUL-1999 (first entry)  
XX  
DE Wild type FRT site DNA.  
XX  
KW FRT; stable transformation; targeted nucleic acid insertion; plant;  
KW chromosome; eukaryotic cell; controlled integration; ss.  
XX  
OS Synthetic.  
XX  
MO9925854-A1.  
PD 27-MAY-1999.  
XX  
PF 17-NOV-1998; 98WO-US24609.  
XX  
PR 18-NOV-1997; 97US-0065627.  
XX  
PR 18-NOV-1997; 97US-0065613.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Baszczynski CL, Gordon-Kamm WJ, Lyznik AL;  
XX  
DR WPI: 1999-347487/29.  
XX  
PT Targeted insertion of nucleic acid into eukaryotic chromosomes  
XX  
PS Disclosure; Page 28; 34pp; English.  
XX  
CC This invention describes a novel method for the targeted insertion of  
CC a nucleic acid sequence into a specific chromosomal site in a eukaryotic  
CC cell. The method is especially used for controlled integration, and  
CC expression, of genes in plants, but may also be applied to mammalian  
CC cells. This method provided efficient integration of a nucleic acid  
CC sequence into predetermined genomic locations, with minimal, if any,  
CC random DNA integration. The use of non-identical recombination sites  
CC prevents recombination between sites and excision of the segment between  
CC them.

XX SQ Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 34; DB 20; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaagtcctatacttctctagagaataggaacttc 34  
Db 34 GAAGTTCCTATCTTCTCTAGAGATAGGAACCTTC 1

RESULT 4

AAK61227/c  
ID AAK61227 standard; DNA; 34 BP.

XX AC AAK61227;

XX 28-JUL-1999 (first entry)

Wild type FRT site.

XX FRT site; directional targeting; gene targeting; plant genome;  
KM non-identical recombination site; chromosomal site; gene stacking;  
KW plant genetic manipulation; ss.

XX Synthetic.

XX WO9925821-A1.

XX 27-MAY-1999.

XX 17-NOV-1998; 98WO-US24610.

XX 18-NOV-1997; 97US-0065627.

XX 18-NOV-1997; 97US-0065613.

XX (PION-) PIONEER HT-BRED INT INC.

XX Baszczynski CL, Bowen BA, Peterson DJ, Tagliani LA;

XX WPI; 1999-347469/29.

XX Directional targeting of desired genes into non-identical  
PT recombination sites in plants

XX PS Disclosure; Page 7; 60pp; English.

CC This sequence represents the wild type FRT recombination site.  
CC The invention relates to a method for the directional targeting of  
CC desired genes into non-identical recombination sites previously  
CC introduced into the target organism's genome (specifically insertion into  
CC a specific chromosomal site within a plant genome), and comprises:  
CC (a) transforming the plant with a transfer cassette that comprises a  
CC nucleotide sequence of interest flanked by non-identical recombination  
CC sites; (b) where the plant genome comprises a target site flanked by  
CC non-identical recombination sites which correspond to the flanking sites  
CC of the transfer cassette; and (c) providing a recombinase that recognises  
CC and implements recombination at the non-identical recombination sites.  
CC The methods are used in targeting the integration of nucleotide sequences  
CC of interest to a specific chromosomal site, finding optimal integration  
CC sites in a plant genome, comparing promoter activity in transformed  
CC plants, engineering chromosomal rearrangements and other genetic  
CC manipulation of plants. The methods allow integration of two or more  
CC genes targeted to the same genomic location, called gene stacking. The  
CC stacked genes can be maintained and managed as a closely linked pair of  
CC traits in breeding programs. Plants amenable to transformation are  
CC monocots, such as maize, or dicots, such as canola, Brassica, soybean,  
CC sunflower and cotton. The methods use novel recombination sites in a gene  
CC targeting system which facilitates directional targeting of desired genes  
CC and nucleotide sequences into corresponding recombination sites  
CC previously introduced into the target plant genome.

XX SQ Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 34; DB 20; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaagtcctatacttctctagagaataggaacttc 34  
Db 34 GAAGTTCCTATCTTCTCTAGAGATAGGAACCTTC 1

RESULT 5

AAK01426/c  
ID AAK01426 standard; DNA; 34 BP.

XX AC AAK01426;

XX 26-APR-1999 (first entry)

XX 2mu FRT element, excision-mediating site.

XX FRT element; excision-mediating site; bacterial artificial chromosome;  
KM ds.  
KW Saccharomyces cerevisiae.

XX US5874259-A.

XX 23-FEB-1999.

XX 21-NOV-1997; 97US-0975763.

XX 21-NOV-1997; 97US-0975763.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Szybalski W;

XX WPI; 1999-179980/15.

XX New improved bacterial artificial chromosome - useful for the  
PT cloning and targeted amplification of large amounts of DNA  
XX Claim 3; Column 15-16; 10pp; English.

CC This sequence represents the yeast 2mu FRT element, which is an  
CC excision-mediating element and can be used in the bacterial artificial  
CC chromosome (BAC) of the invention. The BAC comprises a pair of parallel  
CC excision-mediating sites (EMS) flanking an excisable cloning site that  
CC contains an inducible origin of replication. The improved vectors allow  
CC large amounts of DNA to be selectively obtained from BACs. The improved  
CC BACs employ's amplification and excision systems that negate the need for  
CC interspersing EMS throughout the genome and crossing EMS-containing  
CC strains. The improved BAC provides a system that can be conditionally  
CC induced to excise and amplify the fragment between the EMS.

XX SQ Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 34; DB 20; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaagtcctatacttctctagagaataggaacttc 34  
Db 34 GAAGTTCCTATCTTCTCTAGAGATAGGAACCTTC 1

RESULT 6  
AAK61513/c  
ID AAK61513 standard; DNA; 34 BP.

XX AAC61513;  
AC  
XX 19-FEB-2001 (first entry)  
DT  
XX  
DE Nucleotide sequence of a Flp recognition site.  
XX  
XX translocating protein; cellular process; protein delivery;  
KM Flp recognition site; ss.  
XX  
XX Unidentified.  
OS  
XX WO20005848-A2.  
PN  
XX 05-OCT-2000.  
PD  
XX  
XX 31-MAR-2000; 2000WO-US08571.  
PE  
XX 31-MAR-1999; 99US-0127467.  
PR  
XX (INV1-) INVITROGEN CORP.  
XX  
XX Dalby B, Bennett RP;  
PI  
XX WPI: 2000-6117716/58.  
DR  
XX  
XX Modulating a cellular process by contacting a cell in culture with a  
PT cell process modifying molecule attached to a translocating  
PT polypeptide, useful for modulating expression of a target gene product  
PI  
XX  
XX Disclosure; Page 21; 59pp; English.  
PS  
XX  
XX The present sequence represents a Flp recognition site, which is used  
CC in the course of the invention. The specification describes a method for  
CC modulating a cellular process and for delivery of functional protein  
CC sequences. The method comprises contacting a cell in culture under  
CC suitable conditions with a cell process modifying molecule attached to  
CC a translocating polypeptide, where molecule is translocated into the  
CC cell and interacts specifically with a responsive target site. The  
CC method is useful for modulating a cellular process, such as modulating  
CC expression of a target gene product, of a cell in culture.  
CC  
XX Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;  
SQ

Query Match  
Best Local Similarity 100.0%; Score 34; DB 21; Length 34;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaagttcctatacttctagaagaatagaacttc 34  
|||||  
DB 34 GAAGTTCTCTACTTCTTAGAGAAATAGCACTTC 1

RESULT 7  
AAC63090/c  
ID AAC63090 standard; DNA; 34 BP.  
XX  
AC AAC63090;  
XX  
XX 07-FEB-2001 (first entry)  
DT  
XX  
XX Wild-type FRT site #1.  
DE  
XX  
XX Cre variant recognition site; lox site; recombinase;  
KM variant recombination site; hybrid crop production; seedless crop;  
KM phage packaging; cloning; ds.  
XX  
XX Unidentified.  
OS  
XX WO200060091-A2.  
PN  
XX

PD 12-OCT-2000.  
XX  
XX 06-APR-2000; 2000WO-US09154.  
PE  
XX  
XX 06-APR-1999; 99US-0127977.  
PR  
XX  
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
PA  
XX  
XX Sauer BL, Rufer AW;  
PI  
XX  
XX WPI: 2000-665010/64.  
DR  
XX  
XX Identifying variant recombinases mediating recombination at variant  
PT sites (vrs) by contacting a mutant recombinase, a first and second vrs  
PT having a reporter gene, and a second nucleic acid having 2 vrs and a  
PT reporter gene -  
XX  
XX  
XX Disclosure; Fig 17; 144pp; English.  
PS  
XX  
XX The present invention relates to the identification of recombinase  
CC variants which have an altered specificity. They are tested using  
CC constructs containing variant recognition sites, which are not recognised  
CC by non-mutant recombinase but undergo recombination in the presence of a  
CC variant enzyme. Variant recombinases are useful in the production of a  
CC genetically modified crop plants, particularly seedless varieties, and in  
CC phage packaging, which has uses in cloning.  
CC  
XX Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;  
SQ

Query Match  
Best Local Similarity 100.0%; Score 34; DB 21; Length 34;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaagttcctatacttctagaagaatagaacttc 34  
|||||  
DB 34 GAAGTTCTCTACTTCTTAGAGAAATAGCACTTC 1

RESULT 8  
AAA10237/c  
ID AAA10237 standard; DNA; 34 BP.  
XX  
AC AAA10237;  
XX  
XX 03-JUL-2000 (first entry)  
DT  
XX  
XX Flp recombination target site (FRT).  
DE  
XX  
XX Flp recombination target site; FRT; cell-free subcloning; recombinase;  
KM site-specific recombination; ds.  
KM  
XX Saccharomyces cerevisiae.  
OS  
XX  
XX WO200012687-A1.  
PN  
XX  
XX 09-MAR-2000.  
PD  
XX  
XX 25-AUG-1999; 99WO-US19413.  
PE  
XX  
XX 28-AUG-1998; 98US-0141935.  
PR  
XX  
XX (INV1-) INVITROGEN CORP.  
PA  
XX  
XX Miles DJ, Turner LC, Marcell R, McConnell GC;  
PI  
XX  
XX WPI: 2000-237866/20.  
DR  
XX  
XX Cell free subcloning system for moving nucleic acid sequences from one  
PT type of subcloning vector to another using topoisomerases, contains  
PT donor and acceptor vectors, and a recombinase -  
XX  
XX Claim 7; Page 11; 50pp; English.  
PS

XX The invention relates to a novel cell-free subcloning system comprising a  
 CC donor vector comprising a transfer sequence flanked by site-specific  
 CC recombination sequences, an acceptor vector comprising a site-specific  
 CC recombination sequence that matches that of the donor vector; and a  
 CC site-specific recombinase capable of recognizing the site-specific  
 CC recombination sequences in the vectors. In particular, the recombinase is  
 CC Vaccinia DNA topoisomerase, bacteriophage P1 Cre protein, or  
 CC Saccharomyces cerevisiae FLP. The cell-free subcloning system provides a  
 CC simple, rapid system for the manipulation of nucleic acid sequences  
 CC between vectors. The system also eliminates the need for incorporation of  
 CC add-on base sequences to the transfer sequence to provide unique  
 CC restriction sites. In particular, topoisomerase-based cloning circumvents  
 CC any problems associated with addition of non-templated nucleotides by DNA  
 CC polymerase the 3' end of the amplified DNA. There is also no opportunity  
 CC for the transfer sequences to ligate to one another, which precludes  
 CC cloning of concatameric repeats, and there is no potential for in vitro  
 CC closure of the acceptor vector itself. Additionally, unintended internal  
 CC restriction of an uncharacterised sequence is avoided because the use of  
 CC common restriction enzymes is avoided. The present sequence represents  
 the FLP recombination target site (FRT) which is recognised by the yeast  
 recombinase FLP.

XX Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 34; DB 21; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaagtcctatacttctagagaatagaacttc 34  
 |||||||  
 DB 34 GAAGTCTCTACTTCTTAGAGATAGAACTTC 1

RESULT 9  
 AA258072/c  
 ID AA258072 standard; DNA; 34 BP.

AC AA258072;

DT 25-APR-2000 (first entry)

XX FLP recombinase target site frr.

DE Frr: FLP recombinase: site-specific recombination; subcloning;  
 KM Univector Fusion System; Univector Plasmid-fusion System; ds.  
 XX Saccharomyces cerevisiae.

Key Location/Qualifiers  
 FT repeat\_unit 1..17

FT repeat\_unit /rpt\_type= INVERTED

FT repeat\_unit /tag= a

FT repeat\_unit /rpt\_type= INVERTED

FT repeat\_unit /tag= b

FT repeat\_unit /rpt\_type= INVERTED

FT repeat\_unit /tag= a

FT repeat\_unit /rpt\_type= INVERTED

FT repeat\_unit /tag= b

FT repeat\_unit /rpt\_type= INVERTED

FT repeat\_unit /tag= a

FT repeat\_unit /rpt\_type= INVERTED

FT repeat\_unit /tag= b

PT the rapid subcloning of nucleic acid sequences in vivo and in vitro  
 XX Disclosure: Page 24; 110pp; English.

XX The present sequence is that of the frr site at which the FLP  
 CC recombinase of the 2mu plasmid of Saccharomyces cerevisiae can  
 CC catalyse a site-specific recombination. The frr site can be  
 CC incorporated into vectors of the invention. These novel Univectors,  
 CC or PUN1, have a sequence-specific recombinase target site (e.g. frr)  
 CC preceding the insertion site for the gene of interest, a selectable  
 CC marker gene (optional) and a conditional origin of replication that  
 CC is active only in host cells expressing the requisite transacting  
 CC replication factor (optional). The vectors are designed to contain  
 CC a gene of interest but to lack a promoter for expression of the  
 CC gene. The vectors are used in a novel method for the rapid  
 CC subcloning of nucleic acid sequences in vivo and in vitro without  
 CC the need of restriction endonucleases. The method is referred to  
 CC as the Univector Fusion System or Univector Plasmid-fusion system  
 CC (UPS). The UPS uses site-specific recombination to catalyze plasmid  
 CC fusion between a Univector and host vectors containing regulatory  
 CC information. In some embodiments, plasmid fusion events are  
 CC genetically selected and result in placement of the gene of interest  
 CC under the control of novel regulatory elements. A second UPS-related  
 CC method allows for the precise transfer of coding sequences alone from  
 CC a Univector into a host vector. UPS further provides means for the  
 CC subcloning of entire nucleic acid libraries and the directional  
 CC cloning of linear nucleic acid molecules, e.g. PCR products.

XX Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 34; DB 21; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaagtcctatacttctagagaatagaacttc 34  
 |||||||  
 DB 34 GAAGTCTCTACTTCTTAGAGATAGAACTTC 1

RESULT 10  
 AAD10220/c  
 ID AAD10220 standard; DNA; 34 BP.

AC AAD10220;

DT 24-SEP-2001 (first entry)

XX Minimal wild-type FRT recombination site.

DE Site specific recombinase: expression cassette; FRT recombination site;  
 KM ds.

XX unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

OS unidentified.

PI Baszczynski CL, Lyznik LA, Gordon-Kamm WJ, Guan X, Rao AG;

PI Tagliani LA;  
 XX WPI: 2001-450495/48.  
 DR  
 XX  
 PT Integrating DNA of interest into genome of eukaryotic cell, by  
 PT transforming plant cell with transfer cassette comprising DNA flanked  
 PT by target sites for site-specific recombinases and providing  
 PT recombinases in cell  
 XX  
 PS Disclosure: Column 9: 30pp; English.  
 XX  
 CC The invention relates to compositions and methods for introducing  
 CC a DNA of interest into a genomic target site. The methods and  
 CC compositions involve the use of a combination of target sites for two  
 CC site specific recombinases and expression of a chimeric recombinase  
 CC with dual target site specificity. The compositions comprise novel  
 CC site-specific recombinases with specificities to multiple target sites,  
 CC and nucleotide sequences and expression cassettes encoding these  
 CC recombinases or target sites. The method of integrating foreign DNA  
 CC into genome of eukaryotic cell involves transforming the cell having  
 CC target sites for the novel recombinase with a DNA of interest that is  
 CC flanked by corresponding target sites. The method is useful for  
 CC constructing stably transformed eukaryotic cells, preferably plant  
 CC cells. The present sequence is a minimal wild-type FRT recombination  
 CC site comprising two 13 base pair repeats, separated by an 8 base  
 CC spacer.  
 CC Note: This sequence is incorrectly referred as SEQ.ID.NO.11 in  
 CC Column 11. But this sequence has been designated as SEQ.ID.NO.10 in  
 CC Column 43 of the sequence listing.  
 XX  
 SQ Sequence 34 BP: 11 A; 6 C; 6 G; 11 T; 0 other:  
 Query Match 100.0%; Score 34; DB 22; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 gaagttcctactctctagagaataggaacttc 34  
 Db 34 GAAGTTCCTACTCTTCTAGAGAAATAGCACTTC 1  
 RESULT 11  
 AAH21799  
 ID AAH21799 standard; DNA: 34 BP.  
 XX  
 AC AAH21799;  
 XX  
 OS 15-AUG-2001 (first entry)  
 DE Saccharomyces FRT oligonucleotide sequence SEQ ID NO:1.  
 XX  
 XX Saccharomyces; FRT; yeast; breeding; yeast transformation;  
 KW screening marker gene; galactose inducible proliferation inhibitor;  
 KW FLP recombinase recognition target; brewing beer; ss.  
 XX  
 OS Saccharomyces sp.  
 XX  
 PN WO200131000-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PE 26-OCT-2000; 2000WO-JP07491.  
 XX  
 PR 26-OCT-1999; 99JP-0304185.  
 XX  
 PA (SUNR ) SUNTORY LTD.  
 XX  
 PI Ashikari T, Ochiai M;  
 XX  
 DR WPI: 2001-308637/32.  
 XX  
 PT DNA construct containing a marker gene flanked by excision sequences

PT and a target gene for introduction of multiple copies of the target  
 PT gene into yeast with removal of the marker  
 XX  
 PS Claim 1; Fig 3: 43pp; Japanese.  
 XX  
 CC The present invention describes a DNA construct for yeast transformation,  
 CC containing a screening marker gene and a proliferation inhibitor sequence  
 CC inducible by galactose, flanked by a pair of FLP recombinase recognition  
 CC target (FRT) sequences, and a target gene, the whole being flanked by  
 CC sequences which recombine with yeast chromosomal DNA. Also described  
 CC are: (1) introducing a target gene into yeast by: (a) transforming the  
 CC yeast with the DNA construct; (b) culturing in the absence of galactose  
 CC and selecting for expression of the marker gene; (c) culturing in the  
 CC presence of galactose; and (d) selecting for proliferating yeast, which  
 CC no longer contain the marker gene; and (2) yeast strains transformed by  
 CC the method of (1). The DNA construct can be used for producing  
 CC recombinant yeast strains suitable for use in brewing beer. Multiple  
 CC copies of a target gene can be introduced without accumulation of copies  
 CC of the marker gene. The present sequence represents a specifically  
 CC claimed FRT oligonucleotide sequence for use in a DNA construct of the  
 CC present invention.  
 XX  
 SQ Sequence 34 BP: 11 A; 6 C; 6 G; 11 T; 0 other:  
 Query Match 100.0%; Score 34; DB 22; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 gaagttcctactctctagagaataggaacttc 34  
 Db 1 gaagttcctactctctagagaataggaacttc 34  
 RESULT 12  
 AAF81218/C  
 ID AAF81218 standard; DNA: 34 BP.  
 XX  
 AC AAF81218;  
 XX  
 DT 30-MAY-2001 (first entry)  
 XX  
 DE FLP recombinase recognition sequence FRT.  
 XX  
 XX Yeast; FLP recombinase; fip recognition sequence; FRT;  
 KW adenoviral helper vector; adenovirus; pseudoadenoviral vector;  
 KW PAV vector; gene delivery; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200121824-A1.  
 XX  
 PD 29-MAR-2001.  
 XX  
 PE 14-SEP-2000; 2000WO-US25131.  
 XX  
 PR 23-SEP-1999; 99US-0155758.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 XX  
 PI Romanczuk H, Wadsworth SC, Berthelette P;  
 XX  
 DR WPI: 2001-257997/26.  
 XX  
 PT Novel adenoviral helper vectors which facilitates production and  
 PT packaging of pseudoadenoviral vectors containing reduced levels of  
 PT contaminating helper vector, comprises phage C31 recombinase  
 PT recognition sequences  
 XX  
 PS Example 2; Page 19: 45pp; English.  
 XX  
 CC The present sequence is provided in a specification relating to an  
 CC adenoviral helper vector. The vector comprises an adenovirus

CC genome encoding replication proteins, structural proteins, packaging  
CC elements and adenoviral 5' internal terminal repeat (ITR) sequences  
CC required for the packaging of adenoviral vector particles. It also  
CC comprises phage C1 recombinase nucleotide recognition sequences to  
CC allow for the translocation or excision of the ITR sequences.  
CC The vector is useful in the production of helper-free pseudoviral  
CC (PAV) stocks by providing essential viral proteins in trans for PAV  
CC production and packaging. PAV shuttle vectors are useful for the  
CC delivery of a nucleic acid to a cell for the production of proteins in  
CC vitro and for the in vitro study of proteins in a mammalian system. The  
CC helper vectors, cell lines and PAV are useful for the large scale  
CC commercial production of PAV with minimal contamination by helper  
CC vectors. The helper vectors comprise recombinase nucleotide binding  
CC sites which either excise or rearrange the ITR sequences of the  
CC helper vector to reduce or eliminate helper vector contamination of the  
CC PAV stock. Two copies of the present sequence were placed in an  
CC adenoviral helper construct in an inverted orientation. When this vector  
CC is introduced into Flp-expressing producer cells, the action of the Flp  
CC recombinase on the FRT sequences inverts the central portion of the  
CC vector genome such that the packaging elements are displaced from their  
CC close proximity to the ITR. The packaging elements become embedded  
CC within the genome at a distance which reduces the packaging of the  
CC helper vector such that there is less than 5% contamination of the PAV  
CC preparation.

CC Sequence 34 BP: 11 A; 6 C; 6 G; 11 T; 0 other;

CC Query Match 100.0%; Score 34; DB 22; Length 34;  
CC Best Local Similarity 100.0%; Pred. No. 4e-05;  
CC Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaagtcctactctctctagagaataggaaattc 34  
DB 34 GAAGTTCCTACTCTCTAGAGAATAGGAATCTTC 1

RESULT 13  
AAE24488/C  
ID AAE24488 standard; DNA: 34 BP.

AC AAE24488;

DT 04-MAY-2001 (first entry)

DE Flp recombination target site minimal sequence.

XX Flp recombination target site; FRT; plant genetic modification;  
XX gene integration; gene expression; transfer cassette;  
XX directional integration; ds.

OS Unidentified.

PN US6187994-B1.

PD 13-FEB-2001.

PE 17-NOV-1998; 98US-0193502.

PR 18-NOV-1997; 97US-0065613.

PR 18-NOV-1997; 97US-0065627.

PA (PION-) PIONEER HI-BRED INT INC.

PI Baszczynski CL, Bowen BA, Peterson DJ, Tagliani LA;

DR WPI: 2001-202103/20.

PT Directly selecting transformed plant cells, useful for genetically  
PT modifying or engineering chromosomal rearrangements in plants,  
PT comprises employing novel transfer cassettes and recombination sites in  
PT a gene targeting system

PS Disclosure: Column 5; 20pp; English.

XX The present invention describes a method of selecting transformed plant  
CC cells using novel transfer cassettes and novel minimal recombination  
CC sites in a gene targeting system. This enables the directional  
CC integration of exogenous sequences into a plant's genome. This is useful  
CC for targeting the integration of sequences of interest to a specific  
CC chromosomal site, finding optimal integration sites in a plant genome,  
CC comparing promoter activity in transformed plants, engineering  
CC chromosomal rearrangements and other genetic manipulations of plants. The  
CC present sequence is the Flp recombination target site minimal sequence  
CC (FRT).

CC Sequence 34 BP: 11 A; 6 C; 6 G; 11 T; 0 other;

CC Query Match 100.0%; Score 34; DB 22; Length 34;  
CC Best Local Similarity 100.0%; Pred. No. 4e-05;  
CC Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaagtcctactctctctagagaataggaaattc 34  
DB 34 GAAGTTCCTACTCTCTAGAGAATAGGAATCTTC 1

RESULT 14

AAE87355  
ID AAE87355 standard; DNA: 34 BP.

AC AAE87355;

DT 09-JUL-2001 (first entry)

DE Yeast FRT sequence.

XX Yeast: FRT; gene therapy; gene insertion; gene replacement;  
XX DNA recombination; recombinase; Flp; transgenic animal; ds.

OS Saccharomyces cerevisiae.

PN WO200123545-A1.

PD 05-APR-2001.

PE 28-SEP-2000; 2000WO-JP06686.

PR 30-SEP-1999; 99JP-0280210.

PR 06-DEC-1999; 99JP-0346727.

PA (SUMU) SUMITOMO PHARM CO LTD.

PA (SAIT/) SAITO I.

PI Saito I, Kanegae Y;

DR WPI: 2001-266149/27.

PT Variant FRT sequences useful for in vivo gene therapy comprises central  
PT 8 base spacer sequence

PS Claim 1; Page 41; 73pp; Japanese.

CC The present sequence is an FRT sequence from Saccharomyces  
CC cerevisiae. Variant FRT sequences are provided and may be used in a  
CC method of performing highly efficient gene insertion or gene  
CC replacement. The variant FRT sequences each undergo a recombination  
CC reaction with another variant FRT of the same sequence in the presence  
CC of recombinase Flp. The method is useful for producing transgenic  
CC animal cells and animals. By locally inserting the DNA and recombinase  
CC Flp, genes can be targeted to specific organs or tissues.

CC Sequence 34 BP: 11 A; 6 C; 6 G; 11 T; 0 other;

Query Match 100.0%; Score 34; DB 22; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaagttcctactcttcagagaatagaacttc 34  
 |||  
 Db 1 gaagttcctactcttcagagaatagaacttc 34

## RESULT 15

AAZ06422/c  
 ID AAZ06422 standard; DNA; 35 BP.

XX AAZ06422;  
 AC

XX 09-NOV-1999 (first entry)  
 DT

XX FLP recombinase target (FRT) repeated motif, variant 1.  
 DE

XX FLP recombinase; FLP recombinase target repeated motif; PAV;  
 KM pseudodendoviral; packaging signal; vector; helper virus;  
 packaging cell line; plasmid pOG45; ds.

XX Synthetic.  
 OS

XX Yeast.  
 OS

XX WO9941400-A1.  
 PN

XX 19-AUG-1999.  
 PD

XX 17-FEB-1999; 99WO-US03483.  
 PF

XX 22-MAY-1998; 98US-0086528.  
 PR

XX 17-FEB-1998; 98US-0074761.  
 RX

XX (GENZ ) GENZYME CORP.  
 PA

XX Armeniano D, Gregory RJ, Romanczuk H, Wadsworth SC;  
 PI

XX WPI; 1999-518454/43.  
 DR

XX Novel packaging inhibited pseudodendoviral vector helper virus are  
 PT useful for gene transfer methods

XX Disclosure; Page 11; 65pp; English.  
 PS

XX This is one version of the FLP recombinase target (FRT) repeated motif  
 CC that can be used to catalyze site-specific excision of flanked  
 CC nucleotide sequences. Upon recognition of the FRT nucleotide sequences  
 CC by a FLP recombinase, the flanked packaging signal is excised from the  
 CC helper virus genome, thereby preventing the packaging of the helper  
 CC virus genome and the production of helper virus particles. One reason  
 CC for using FLP recombinase is because it exhibits increased  
 CC thermostability at 37 degrees C.

XX Sequence 35 BP; 11 A; 7 C; 6 G; 11 T; 0 other;  
 SQ

Query Match 100.0%; Score 34; DB 20; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 35 GAAGTTCTATACCTTCTAGAGAAATAGAACTTC 2-

Search completed: December 14, 2001, 19:26:36  
 Job time: 18231 sec

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	100.0	34	6	AS9775	AS9775 Sequence 2
2	34	100.0	34	6	AR067801	AR067801 Sequence
3	34	100.0	34	6	AR105498	AR105498 Sequence
4	34	100.0	34	6	AR130339	AR130339 Sequence
5	34	100.0	34	6	AR142481	AR142481 Sequence
6	34	100.0	34	6	AX101007	AX101007 Sequence
7	34	100.0	34	6	IS5685	IS5685 Sequence 3
8	34	100.0	34	6	IS9353	IS9353 Sequence 3
9	34	100.0	54	6	AR003616	AR003616 Sequence
10	34	100.0	54	6	AR071165	AR071165 Sequence
11	34	100.0	54	6	AR108166	AR108166 Sequence
12	34	100.0	54	6	I23383	I23383 Sequence 9
13	34	100.0	61	6	E15549	E15549 DNA encodin
14	34	100.0	68	6	I08526	I08526 Sequence 1
15	34	100.0	68	6	I59686	I59686 Sequence 4
16	34	100.0	68	6	I69354	I69354 Sequence 4
17	34	100.0	69	6	AR130340	AR130340 Sequence
18	34	100.0	121	12	APDNKTSR2	X87981 Artificial
19	34	100.0	125	12	APDNKTSR3	X87982 Artificial
20	34	100.0	144	8	PZMF1P	M33380 Saccharomyc
21	34	100.0	154	12	APDNKTSR1	X87980 Artificial
22	34	100.0	200	8	YSCPL2M	K01710 Yeast (S.c
23	34	100.0	1019	8	SCPL1	K01322 Part of the
24	34	100.0	1340	6	AR066336	AR066336 Sequence
25	34	100.0	1578	8	SCOR01	V01317 Yeast sequ
26	34	100.0	1814	12	CYPMKAK76	U08460 Cloning vec
27	34	100.0	1842	12	ASPSG76K	Y09894 Suicide pla
28	34	100.0	1888	12	CYPMKAC76	U08461 Cloning vec
29	34	100.0	1916	12	ASPSG76C	Y09893 Suicide pla
30	34	100.0	1929	6	AX097927	AX097927 Sequence
31	34	100.0	1939	12	AF172934	AF172934 Integrati
32	34	100.0	2003	6	AX097928	AX097928 Sequence
33	34	100.0	2003	12	AF172935	AF172935 Integrati
34	34	100.0	2340	12	ASPSG76A	Y09892 Suicide pla
35	34	100.0	2427	6	AX097926	AX097926 Sequence
36	34	100.0	2427	12	AF172933	AF172933 Integrati
37	34	100.0	3159	12	ASPS76A	Y09895 Suicide pla
38	34	100.0	3246	6	AX097929	AX097929 Sequence
39	34	100.0	3246	12	AF172936	AF172936 Integrati
40	34	100.0	3356	12	ASPS76K	Y09897 Suicide pla
41	34	100.0	3421	12	ASPS76C	Y09896 Suicide pla
42	34	100.0	3443	6	AX097930	AX097930 Sequence
43	34	100.0	3443	12	AF172937	AF172937 Integrati
44	34	100.0	3508	6	AX097931	AX097931 Sequence
45	34	100.0	3508	12	AF172938	AF172938 Integrati

RESULT	1				
LOCUS	A59775				
DEFINITION	Sequence 2 from Patent WO9705255.				
ACCESSION	A59775				
VERSION	A59775.1				
KEYWORDS	GI:3715001				
SOURCE	unidentified.				
ORGANISM	unidentified				
REFERENCE	unclassified.				
AUTHORS	1 (bases 1 to 34)				
TITLE	Lusky, M. and Mehal, M.				
JOURNAL	HELPER VIRUSES FOR PREPARING RECOMBINANT VIRAL VECTORS				
COMMENT	Patent: WO 9705255-A 2 13-FEB-1997;				
FEATURES	TRANSGENE SA (PR)				
Source	Other publication FR 2737501 970207.				
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	/organism="unidentified"				
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BASE COUNT 11 a /db\_xref="taxon:32644" 6 c 11 t  
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Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAGTTCCTATACCTTCTAGAGAAATAGCAACTTC 34

RESULT 2  
LOCUS AR067801 34 bp DNA  
DEFINITION Sequence 18 from patent US 5851808.  
ACCESSION AR067801  
VERSION AR067801.1 GI:5999023  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Elledge,S.J. and Liu,Q.  
TITLE Rapid subcloning using site-specific recombination  
JOURNAL Patent: US 5851808-A 18 22-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..34

BASE COUNT 11 a /organism="unknown" 6 c 11 t  
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Query Match 100.0% Score 34; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gaagtcctatactctcagagaataggaacttc 34  
Db 34 GAAGTTCCTATACCTTCTAGAGAAATAGCAACTTC 1

RESULT 3  
LOCUS AR105498 34 bp DNA  
DEFINITION Sequence 5 from patent US 6096717.  
ACCESSION AR105498  
VERSION AR105498.1 GI:12819095  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Jarvik,J.W.  
TITLE Method for producing tagged genes transcripts and proteins  
JOURNAL Patent: US 6096717-A 5 01-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..34

BASE COUNT 11 a /organism="unknown" 6 c 11 t  
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Query Match 100.0% Score 34; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 34 GAAGTTCCTATACCTTCTAGAGAAATAGCAACTTC 1

RESULT 4  
LOCUS AR130339 34 bp DNA  
DEFINITION Sequence 1 from patent US 6187994.  
ACCESSION AR130339  
VERSION AR130339.1 GI:14118236  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Baszczyński,C.L., Bowen,B.A., Peterson,D.J. and Tagliani,L.A.  
TITLE Compositions and methods for genetic modification of plants  
JOURNAL Patent: US 6187994-A 1 13-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..34

BASE COUNT 11 a /organism="unknown" 6 c 11 t  
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Query Match 100.0% Score 34; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
LOCUS AR142481 34 bp DNA  
DEFINITION Sequence 4 from patent US 6175058.  
ACCESSION AR142481  
VERSION AR142481.1 GI:15102780  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Baszczyński,C.L., Bowen,B.A., Drummond,B.J., Gordon-Kamm,W.J., Peterson,D.J., Sandahl,G.A., Tagliani,L.A., Zhao,Z.-Y. and St. Clair,Gmarie.  
TITLE Nucleic acid sequence encoding FLP recombinase  
JOURNAL Patent: US 6175058-A 4 16-JAN-2001;  
FEATURES Location/Qualifiers  
source 1..34

BASE COUNT 11 a /organism="unknown" 6 c 11 t  
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RESULT 6  
LOCUS AX101007 34 bp DNA  
DEFINITION Sequence 1 from Patent W00121024.  
ACCESSION AX101007  
VERSION AX101007.1 GI:13619864  
KEYWORDS  
SOURCE baker's yeast.  
ORGANISM Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

REFERENCE Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
1 (bases 1 to 34)

AUTHORS Romanczuk, H., Wadsworth, S.C. and Berthelotte, P.  
TITLE Helper vectors and cell lines for the production of  
pseudodendroviral vectors

JOURNAL Patent: WO 0121824-A 1 29-MAR-2001;  
GENZYME CORPORATION (US)  
FEATURES Location/Qualifiers

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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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34 GAAGTTCCTACTTCTTAGAGAAATAGGAACCTTC 1

RESULT 7  
LOCUS 159685 34 bp DNA PAT 07-OCT-1997  
DEFINITION Sequence 3 from patent US 5654182.  
ACCESSION 159685  
VERSION 159685.1 GI:2478317  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Wahl, G.M. and O'Gorman, S.V.  
TITLE FLP-mediated gene modification in mammalian cells, and compositions  
and cells useful therefor

JOURNAL Patent: US 5654182-A 3 05-AUG-1997;  
FEATURES Location/Qualifiers

source 1..34  
/organism="unknown"

BASE COUNT 11 a 6 c 6 g 11 t  
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Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 34 GAAGTTCCTACTTCTTAGAGAAATAGGAACCTTC 1

RESULT 8  
LOCUS 169353 34 bp DNA PAT 04-FEB-1998  
DEFINITION Sequence 3 from patent US 5677177.  
ACCESSION 169353  
VERSION 169353.1 GI:2831475  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Wahl, G.M. and O'Gorman, S.V.  
TITLE FLP-mediated gene modification in mammalian cells, and compositions  
and cells useful therefor

JOURNAL Patent: US 5677177-A 3 14-OCT-1997;  
FEATURES Location/Qualifiers

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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9  
LOCUS AR003616 54 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 9 from patent US 5744336.  
ACCESSION AR003616  
VERSION AR003616.1 GI:3964875  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 54)  
AUTHORS Hodges, T.K. and Lyznik, L.A.  
TITLE DNA constructs for controlled transformation of eukaryotic cells  
JOURNAL Patent: US 5744336-A 9 28-APR-1998;  
FEATURES Location/Qualifiers

source 1..54  
/organism="unknown"

BASE COUNT 18 a 9 c 11 g 16 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 GAAGTTCCTACTTCTTAGAGAAATAGGAACCTTC 39

RESULT 10  
LOCUS AR071165 54 bp DNA PAT 18-FEB-2000  
DEFINITION Sequence 9 from patent US 5910415.  
ACCESSION AR071165  
VERSION AR071165.1 GI:7222053  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 54)  
AUTHORS Hodges, T.K. and Lyznik, L.A.  
TITLE Controlled modification of eukaryotic genomes  
JOURNAL Patent: US 5910415-A 9 08-JUN-1999;  
FEATURES Location/Qualifiers

source 1..54  
/organism="unknown"

BASE COUNT 18 a 9 c 11 g 16 t  
ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 GAAGTTCCTACTTCTTAGAGAAATAGGAACCTTC 39

RESULT 11  
LOCUS ARI08166 54 bp DNA  
DEFINITION Sequence 9 from patent US 6110736.  
ACCESSION ARI08166  
VERSION ARI08166.1 GI:12823653  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Hodges,T.K. and Lyznik,L.A.  
TITLE Site-directed recombination in plants  
JOURNAL Patent: US 6110736-A 9 29-AUG-2000;  
FEATURES  
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BASE COUNT 18 a 9 c 11 g 16 t  
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DB 6 GAAGTTCCTACTTCTTAGAGAAATAGCAACTTC 39

RESULT 12  
LOCUS 122383 54 bp DNA  
DEFINITION Sequence 9 from patent US 5527695.  
ACCESSION 122383  
VERSION 122383.1 GI:1602737  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Hodges,T.K. and Lyznik,L.A.  
TITLE Controlled modification of eukaryotic genomes  
JOURNAL Patent: US 5527695-A 9 18-JUN-1996;  
FEATURES  
source 1..54  
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BASE COUNT 18 a 9 c 11 g 16 t  
ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaagtcctatactctctagagaataggaacttc 34  
DB 6 GAAGTTCCTACTTCTTAGAGAAATAGCAACTTC 39

RESULT 13  
LOCUS E15549 61 bp DNA  
DEFINITION DNA encoding Flp Recombination Target (FRT).  
ACCESSION E15549  
VERSION E15549.1 GI:5710232  
KEYWORDS JP 1996075790-A/1.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 61)  
AUTHORS Tomita,H., Imanishi,S., Tamura,T. and Hata,T.  
TITLE VECTOR FOR TRANSFECTING EXTRANEOUS GENE TO INSECT CELL

JOURNAL  
COMMENT Patent: JP 1998075790-A 1 24-MAR-1998;  
NORIN SUISANSYO SANSHI KONCHU NOGIO GIJUTSU KENKYUSHO  
OS Unknown  
PN JP 1998075790-A/1  
PD 24-MAR-1998  
PF 05-SEP-1996 JP 1996235290  
PI TOMITA HIDECHIRO, IMANISHI SHIGEO, TAMURA TOSHIKI, PI HATA  
TAMAKO  
PC C12N15/09,C07H21/04,C12N5/10/C12P21/02,C12N5/10,C12R1:91),  
PC (C12P21/02,  
PC C12R1:91);  
CC Strandedness: Double;  
CC Topology: Linear;  
CC Hypothetical: No;  
CC anti-sense: No;  
FH Key location/Qualifiers  
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FT /organism="unclassified"  
FT misc\_feature 1..61  
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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GAAGTTCCTACTTCTTAGAGAAATAGCAACTTC 28

RESULT 14  
LOCUS 108526 68 bp DNA  
DEFINITION Sequence 1 from Patent WO 8703006.  
ACCESSION 108526  
VERSION 108526.1 GI:588764  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 68)  
AUTHORS Rogers,D.T. and Szostak,J.W.  
TITLE YEAST STRAINS  
JOURNAL Patent: WO 8703006-A 1 21-MAY-1987;  
FEATURES  
source 1..68  
Location/Qualifiers  
/organism="unknown"  
BASE COUNT 18 a 15 c 13 g 22 t  
ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 68;  
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DB 58 GAAGTTCCTACTTCTTAGAGAAATAGCAACTTC 25

RESULT 15  
LOCUS I59686 68 bp DNA  
DEFINITION Sequence 4 from patent US 5654182.  
ACCESSION I59686

VERSION I59686.1 GI:2478318  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 68)  
 AUTHORS Wahl, G.M. and O'Gorman, S.V.  
 TITLE FLP-mediated gene modification in mammalian cells, and compositions  
 and cells useful therefor  
 JOURNAL Patent: US 5654182-A 4 05-AUG-1997;  
 FEATURES Location/Qualifiers  
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Search completed: December 14, 2001, 19:23:40  
 Job time: 19480 sec

